



#12/B

1/10

## SEQUENCE LISTING

<110> Chen, Li How  
Meade, Henry

<120> NOVEL MODIFIED MSP-1 NUCLEIC ACID SEQUENCES AND METHODS  
FOR INCREASING mRNA LEVELS AND PROTEIN EXPRESSIONS IN  
CELL SYSTEMS

<130> 10275/134001

<140> US 09/175,683

<141> 1998-10-20

<150> US 60/095,649

<151> 1998-08-07

<150> US 60/062,592

<151> 1997-10-20

<160> 13

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1065

<212> DNA

<213> preferably, a bacterium, virus, or parasite

<220>

<221> CDS

<222> (1)...(1065)

<400> 1

gcc gtc act ccc tcc gtc atc gat aac atc ctg tcc aag atc gag aac 48  
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1 5 10 15

gag tac gag gtg ctg tac ctg aag ccg ctg gca ggg gtc tac cgg agc 96  
Glu Tyr Glu Val Leu Tyr Leu Lys Pro Leu Ala Gly Val Tyr Arg Ser  
20 25 30

ctg aag aag cag ctg gag aac aac gtg atg acc ttc aac gtg aac gtg 144  
Leu Lys Lys Gln Leu Glu Asn Asn Val Met Thr Phe Asn Val Asn Val  
35 40 45

aag gat atc ctg aac agc cgg ttc aac aag cgg gag aac ttc aag aac 192  
Lys Asp Ile Leu Asn Ser Arg Phe Asn Lys Arg Glu Asn Phe Lys Asn  
50 55 60

gtg ctg gag agc gat ctg atc ccc tac aag gat ctg acc agc agc aac 240  
Val Leu Glu Ser Asp Leu Ile Pro Tyr Lys Asp Leu Thr Ser Ser Asn  
65 70 75 80

tac gtg gtc aag gat ccc tac aag ttc ctg aac aag gag aag aga gat 288  
Tyr Val Val Lys Asp Pro Tyr Lys Phe Leu Asn Lys Glu Lys Arg Asp  
85 90 95

aag ttc ctg agc agt tac aac tac atc aag gat agc att gat acc gat 336  
Lys Phe Leu Ser Ser Tyr Asn Tyr Ile Lys Asp Ser Ile Asp Thr Asp  
100 105 110

B1

|   |      |
|---|------|
| atc aac ttc gcc aac gat gtc ctg gga tac tac aag atc ctg tcc gag<br>Ile Asn Phe Ala Asn Asp Val Leu Gly Tyr Tyr Lys Ile Leu Ser Glu<br>115 120 125     | 384  |
| aag tac aag agc gat ctg gat tca atc aag aag tac atc aac gat aag<br>Lys Tyr Lys Ser Asp Leu Asp Ser Ile Lys Lys Tyr Ile Asn Asp Lys<br>130 135 140     | 432  |
| cag gga gag aac gag aag tac ctg ccc ttc ctg aac aac atc gag acc<br>Gln Gly Glu Asn Glu Lys Tyr Leu Pro Phe Leu Asn Asn Ile Glu Thr<br>145 150 155 160 | 480  |
| ctg tac aag acc gtc aac gat aag att gat ctg ttc gtg atc cac ctg<br>Leu Tyr Lys Thr Val Asn Asp Lys Ile Asp Leu Phe Val Ile His Leu<br>165 170 175     | 528  |
| gag gcc aag gtc ctg aac tac aca tat gag aag agc aac gtg gag gtc<br>Glu Ala Lys Val Leu Asn Tyr Thr Tyr Glu Lys Ser Asn Val Glu Val<br>180 185 190     | 576  |
| aag atc aag gag ctg aat tac ctg aag acc atc cag gat aag ctg gcc<br>Lys Ile Lys Glu Leu Asn Tyr Leu Lys Thr Ile Gln Asp Lys Leu Ala<br>195 200 205     | 624  |
| gat ttc aag aag aac aac aac ttc gtc ggg atc gcc gat ctg agc acc<br>Asp Phe Lys Lys Asn Asn Asn Phe Val Gly Ile Ala Asp Leu Ser Thr<br>210 215 220     | 672  |
| gat tac aac cac aac aac ctg ctg acc aag ttc ctg agc acc ggt atg<br>Asp Tyr Asn His Asn Asn Leu Leu Thr Lys Phe Leu Ser Thr Gly Met<br>225 230 235 240 | 720  |
| gtc ttc gaa aac ctg gcc aag acc gtc ctg agc aac ctg ctg gat ggg<br>Val Phe Glu Asn Leu Ala Lys Thr Val Leu Ser Asn Leu Leu Asp Gly<br>245 250 255     | 768  |
| aac ctg cag ggg atg ctg aac atc agc cag cac cag tgt gtg aag aag<br>Asn Leu Gln Gly Met Leu Asn Ile Ser Gln His Gln Cys Val Lys Lys<br>260 265 270     | 816  |
| cag tgt ccc cag aac agc ggg tgt ttc aga cac ctg gat gag aga gag<br>Gln Cys Pro Gln Asn Ser Gly Cys Phe Arg His Leu Asp Glu Arg Glu<br>275 280 285     | 864  |
| gag tgt aag tgt ctg ctg aac tac aag cag gaa ggt gat aag tgt gtg<br>Glu Cys Lys Cys Leu Leu Asn Tyr Lys Gln Glu Gly Asp Lys Cys Val<br>290 295 300     | 912  |
| gaa aac ccc aat cct act tgt aac gag aac aat ggt gga tgt gat gcc<br>Glu Asn Pro Asn Pro Thr Cys Asn Glu Asn Asn Gly Gly Cys Asp Ala<br>305 310 315 320 | 960  |
| gat gcc aag tgt acc gag gag gat tca ggg agc aac ggg aag aag atc<br>Asp Ala Lys Cys Thr Glu Glu Asp Ser Gly Ser Asn Gly Lys Lys Ile<br>325 330 335     | 1008 |
| acc tgt gag tgt acc aag cct gat tct tat cca ctg ttc gat ggt atc<br>Thr Cys Glu Cys Thr Lys Pro Asp Ser Tyr Pro Leu Phe Asp Gly Ile<br>340 345 350     | 1056 |

B1  
cont.

ttc tgt agt  
Phe Cys Ser  
355

1065

&lt;210&gt; 2

&lt;211&gt; 1088

&lt;212&gt; DNA

&lt;213&gt; preferably, a bacterium, virus, or parasite

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1083)

&lt;400&gt; 2

gca gta act cct tcc gta att gat aac ata ctt tct aaa att gaa aat 48  
Ala Val Thr Pro Ser Val Ile Asp Asn Ile Leu Ser Lys Ile Glu Asn  
1 5 10 15

gaa tat gag gtt tta tat tta aaa cct tta gca ggt gtt tat aga agt 96  
Glu Tyr Glu Val Leu Tyr Leu Lys Pro Leu Ala Gly Val Tyr Arg Ser  
20 25 30

tta aaa aaa caa tta gaa aat aac gtt atg aca ttt aat gtt aat gtt 144  
Leu Lys Lys Gln Leu Glu Asn Asn Val Met Thr Phe Asn Val Asn Val  
35 40 45

aag gat att tta aat tca cga ttt aat aaa cgt gaa aat ttc aaa aat 192  
Lys Asp Ile Leu Asn Ser Arg Phe Asn Lys Arg Glu Asn Phe Lys Asn  
50 55 60

gtt tta gaa tca gat tta att cca tat aaa gat tta aca tca agt aat 240  
Val Leu Glu Ser Asp Leu Ile Pro Tyr Lys Asp Leu Thr Ser Ser Asn  
65 70 75 80

tat gtt gtc aaa gat cca tat aaa ttt ctt aat aaa gaa aaa aga gat 288  
Tyr Val Val Lys Asp Pro Tyr Lys Phe Leu Asn Lys Glu Lys Arg Asp  
85 90 95

aaa ttc tta agc agt tat aat tat att aag gat tca ata gat acg gat 336  
Lys Phe Leu Ser Ser Tyr Asn Tyr Ile Lys Asp Ser Ile Asp Thr Asp  
100 105 110

ata aat ttt gca aat gat gtt ctt gga tat tat aaa ata tta tcc gaa 384  
Ile Asn Phe Ala Asn Asp Val Leu Gly Tyr Tyr Lys Ile Leu Ser Glu  
115 120 125

aaa tat aaa tca gat tta gat tca att aaa aaa tat atc aac gac aaa 432  
Lys Tyr Lys Ser Asp Leu Asp Ser Ile Lys Lys Tyr Ile Asn Asp Lys  
130 135 140

caa ggt gaa aat gag aaa tac ctt ccc ttt tta aac aat att gag acc 480  
Gln Gly Glu Asn Glu Lys Tyr Leu Pro Phe Leu Asn Asn Ile Glu Thr  
145 150 155 160

tta tat aaa aca gtt aat gat aaa att gat tta ttt gta att cat tta 528  
Leu Tyr Lys Thr Val Asn Asp Lys Ile Asp Leu Phe Val Ile His Leu  
165 170 175

Cont.

4/10

|   |      |
|---|------|
| gaa gca aaa gtt cta aat tat aca tat gag aaa tca aac gta gaa gtt<br>Glu Ala Lys Val Leu Asn Tyr Thr Tyr Glu Lys Ser Asn Val Glu Val<br>180 185 190     | 576  |
| aaa ata aaa gaa ctt aat tac tta aaa aca att caa gac aaa ttg gca<br>Lys Ile Lys Glu Leu Asn Tyr Leu Lys Thr Ile Gln Asp Lys Leu Ala<br>195 200 205     | 624  |
| gat ttt aaa aaa aat aac aat ttc gtt gga att gct gat tta tca aca<br>Asp Phe Lys Lys Asn Asn Asn Phe Val Gly Ile Ala Asp Leu Ser Thr<br>210 215 220     | 672  |
| gat tat aac cat aat aac tta ttg aca aag ttc ctt agt aca ggt atg<br>Asp Tyr Asn His Asn Asn Leu Leu Thr Lys Phe Leu Ser Thr Gly Met<br>225 230 235 240 | 720  |
| gtt ttt gaa aat ctt gct aaa acc gtt tta tct aat tta ctt gat gga<br>Val Phe Glu Asn Leu Ala Lys Thr Val Leu Ser Asn Leu Leu Asp Gly<br>245 250 255     | 768  |
| aac ttg caa ggt atg tta aac att tca caa cac caa tgc gta aaa aaa<br>Asn Leu Gln Gly Met Leu Asn Ile Ser Gln His Gln Cys Val Lys Lys<br>260 265 270     | 816  |
| caa tgt cca caa aat tct gga tgt ttc aga cat tta gat gaa aga gaa<br>Gln Cys Pro Gln Asn Ser Gly Cys Phe Arg His Leu Asp Glu Arg Glu<br>275 280 285     | 864  |
| gaa tgt aaa tgt tta tta aat tac aaa caa gaa ggt gat aaa tgt gtt<br>Glu Cys Lys Cys Leu Leu Asn Tyr Lys Gln Glu Gly Asp Lys Cys Val<br>290 295 300     | 912  |
| gaa aat cca aat cct act tgt aac gaa aat aat ggt gga tgt gat gca<br>Glu Asn Pro Asn Pro Thr Cys Asn Glu Asn Asn Gly Gly Cys Asp Ala<br>305 310 315 320 | 960  |
| gat gcc aaa tgt acc gaa gaa gat tca ggt agc aac gga aag aaa atc<br>Asp Ala Lys Cys Thr Glu Glu Asp Ser Gly Ser Asn Gly Lys Lys Ile<br>325 330 335     | 1008 |
| aca tgt gaa tgt act aaa cct gat tct tat cca ctt ttc gat ggt att<br>Thr Cys Glu Cys Thr Lys Pro Asp Ser Tyr Pro Leu Phe Asp Gly Ile<br>340 345 350     | 1056 |
| ttc tgc agt cac cac cac cac cac cac taact<br>Phe Cys Ser His His His His His His<br>355 360   | 1088 |

<210> 3

<211> 88

<212> DNA

<213> preferably, a bacterium, virus, or parasite

<400> 3

tcgacgagag ccatgaaggt cctcatcctt gcctgtctgg tggctctggc cattgcaaga  
gagcaggaag aactcaatgt agtcggtta

60

88

<210> 4

<211> 88

<212> DNA

<213> preferably, a bacterium, virus, or parasite

B1  
cont

<400> 4  
 gatctaccga ctacattgag ttcttctctgc tctcttgcaa tggccagagc caccagacag 60  
 gcaaggatga ggaccttcat ggctctcg 88

<210> 5  
 <211> 60  
 <212> DNA  
 <213> preferably, a bacterium, virus, or parasite

<400> 5  
 taactcgagc gaaccatgaa ggtcctcatc cttgcctgtc tgggtggctct ggccattgca 60

<210> 6  
 <211> 48  
 <212> DNA  
 <213> preferably, a bacterium, virus, or parasite

<400> 6  
 aattctcgag ttagtggtgg tgggtgggtg gactgcagaa ataccatc 48

<210> 7  
 <211> 31  
 <212> DNA  
 <213> preferably, a bacterium, virus, or parasite

<400> 7  
 aatagatctg cagtaactcc ttccgtaatt g 31

<210> 8  
 <211> 1142  
 <212> DNA  
 <213> preferably, a bacterium, virus, or parasite

<220>  
 <221> CDS  
 <222> (1)...(1128)

<400> 8  
 atg aag gtc ctc ata att gcc tgt ctg gtg gct ctg gcc att gca gcc 48  
 Met Lys Val Leu Ile Ile Ala Cys Leu Val Ala Leu Ala Ile Ala Ala  
 1 5 10 15

gtc act ccc tcc gtc atc gat aac atc ctg tcc aag atc gag aac gag 96  
 Val Thr Pro Ser Val Ile Asp Asn Ile Leu Ser Lys Ile Glu Asn Glu  
 20 25 30

tac gag gtg ctg tac ctg aag ccc ctg gca gga gtc tac agg agc ctg 144  
 Tyr Glu Val Leu Tyr Leu Lys Pro Leu Ala Gly Val Tyr Arg Ser Leu  
 35 40 45

aag aag cag ctg gag aac aac gtg atg acc ttc aac gtg aac gtg aag 192  
 Lys Lys Gln Leu Glu Asn Asn Val Met Thr Phe Asn Val Asn Val Lys  
 50 55 60

gat atc ctg aac agc agg ttc aac aag agg gag aac ttc aag aac gtg 240  
 Asp Ile Leu Asn Ser Arg Phe Asn Lys Arg Glu Asn Phe Lys Asn Val  
 65 70 75 80

ctg gag agc gat ctg atc ccc tac aag gat ctg acc agc agc aac tac 288  
 Leu Glu Ser Asp Leu Ile Pro Tyr Lys Asp Leu Thr Ser Ser Asn Tyr  
 85 90 95

*BiCont.*

gtg gtc aaa gat ccc tac aag ttc ctg aac aag gag aag aga gat aag 336  
 Val Val Lys Asp Pro Tyr Lys Phe Leu Asn Lys Glu Lys Arg Asp Lys  
 100 105 110

ttc ctg agc agt tac aat tac atc aag gat agc att gac acc gat atc 384  
 Phe Leu Ser Ser Tyr Asn Tyr Ile Lys Asp Ser Ile Asp Thr Asp Ile  
 115 120 125

aac ttc gcc aac gat gtc ctg gga tac tac aag atc ctg tcc gag aag 432  
 Asn Phe Ala Asn Asp Val Leu Gly Tyr Tyr Lys Ile Leu Ser Glu Lys  
 130 135 140

tac aag agc gat ctg gat agc atc aag aag tac atc aac gat aag cag 480  
 Tyr Lys Ser Asp Leu Asp Ser Ile Lys Lys Tyr Ile Asn Asp Lys Gln  
 145 150 155 160

gga gag aac gag aag tac ctg ccc ttc ctg aac aac atc gag acc ctg 528  
 Gly Glu Asn Glu Lys Tyr Leu Pro Phe Leu Asn Asn Ile Glu Thr Leu  
 165 170 175

tac aag acc gtc aac gat aag att gat ctg ttc gtg atc cac ctg gag 576  
 Tyr Lys Thr Val Asn Asp Lys Ile Asp Leu Phe Val Ile His Leu Glu  
 180 185 190

gcc aag gtc ctg cag tac aca tat gag aag agc aac gtg gag gtc aag 624  
 Ala Lys Val Leu Gln Tyr Thr Tyr Glu Lys Ser Asn Val Glu Val Lys  
 195 200 205

atc aag gag ctg aat tac ctg aag acc atc cag gat aag ctg gcc gat 672  
 Ile Lys Glu Leu Asn Tyr Leu Lys Thr Ile Gln Asp Lys Leu Ala Asp  
 210 215 220

ttc aag aag aac aac aac ttc gtc gga atc gcc gat ctg agc acc gat 720  
 Phe Lys Lys Asn Asn Asn Phe Val Gly Ile Ala Asp Leu Ser Thr Asp  
 225 230 235 240

tac aac cac aac aac ctg ctg acc aag ttc ctg agc acc gga atg gtc 768  
 Tyr Asn His Asn Asn Leu Leu Thr Lys Phe Leu Ser Thr Gly Met Val  
 245 250 255

ttc gaa aac ctg gcc aag acc gtc ctg agc aac ctg ctg gat gga aac 816  
 Phe Glu Asn Leu Ala Lys Thr Val Leu Ser Asn Leu Leu Asp Gly Asn  
 260 265 270

ctg cag gga atg ctg cag atc agc cag cac cag tgt gtg aag aag cag 864  
 Leu Gln Gly Met Leu Gln Ile Ser Gln His Gln Cys Val Lys Lys Gln  
 275 280 285

tgt ccc cag aac agc gga tgc ttc aga cac ctg gat gag agg gag gag 912  
 Cys Pro Gln Asn Ser Gly Cys Phe Arg His Leu Asp Glu Arg Glu Glu  
 290 295 300

tgc aag tgc ctg ctg aac tac aag cag gaa gga gat aag tgt gtg gaa 960  
 Cys Lys Cys Leu Leu Asn Tyr Lys Gln Glu Gly Asp Lys Cys Val Glu  
 305 310 315 320

aac ccc aat cct act tgt aac gag aac aat gga gga tgc gat gcc gat 1008  
 Asn Pro Asn Pro Thr Cys Asn Glu Asn Asn Gly Gly Cys Asp Ala Asp  
 325 330 335

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gcc aag tgt acc gag gag gat tca gga agc aac gga aag aag atc acc 1056  
 Ala Lys Cys Thr Glu Glu Asp Ser Gly Ser Asn Gly Lys Lys Ile Thr  
                   340                  345                  350

tgc gag tgt acc aag cct gat tct tat cca ctg ttc gat ggt att ttc 1104  
 Cys Glu Cys Thr Lys Pro Asp Ser Tyr Pro Leu Phe Asp Gly Ile Phe  
                   355                  360                  365

tgc agt cac cac cac cac cac cac taactcgagg atcc 1142  
 Cys Ser His His His His His His  
           370                  375

<210> 9

<211> 82

<212> DNA

<213> preferably, a bacterium, virus, or parasite

<400> 9  
 ggccgctcga cgccaccatg aaggtcctca taattgctg tctggtggct ctggccattg 60  
 cagccgtcac tcctccgtc at 82

<210> 10

<211> 80

<212> DNA

<213> preferably, a bacterium, virus, or parasite

<400> 10  
 cgatgacgga gggagtgcg gctgcaatgg ccagagccac cagacaggca attatgagga 60  
 ccttcattggt ggcgtcgagc 80

<210> 11

<211> 355

<212> PRT

<213> preferably, a bacterium, virus, or parasite

<400> 11  
 Ala Val Thr Pro Ser Val Ile Asp Asn Ile Leu Ser Lys Ile Glu Asn  
   1                  5                  10                  15  
 Glu Tyr Glu Val Leu Tyr Leu Lys Pro Leu Ala Gly Val Tyr Arg Ser  
                   20                  25                  30  
 Leu Lys Lys Gln Leu Glu Asn Asn Val Met Thr Phe Asn Val Asn Val  
                   35                  40                  45  
 Lys Asp Ile Leu Asn Ser Arg Phe Asn Lys Arg Glu Asn Phe Lys Asn  
                   50                  55                  60  
 Val Leu Glu Ser Asp Leu Ile Pro Tyr Lys Asp Leu Thr Ser Ser Asn  
                   65                  70                  75                  80  
 Tyr Val Val Lys Asp Pro Tyr Lys Phe Leu Asn Lys Glu Lys Arg Asp  
                   85                  90                  95  
 Lys Phe Leu Ser Ser Tyr Asn Tyr Ile Lys Asp Ser Ile Asp Thr Asp  
                   100                  105                  110  
 Ile Asn Phe Ala Asn Asp Val Leu Gly Tyr Tyr Lys Ile Leu Ser Glu  
                   115                  120                  125  
 Lys Tyr Lys Ser Asp Leu Asp Ser Ile Lys Lys Tyr Ile Asn Asp Lys  
                   130                  135                  140  
 Gln Gly Glu Asn Glu Lys Tyr Leu Pro Phe Leu Asn Asn Ile Glu Thr  
                   145                  150                  155                  160  
 Leu Tyr Lys Thr Val Asn Asp Lys Ile Asp Leu Phe Val Ile His Leu  
                   165                  170                  175  
 Glu Ala Lys Val Leu Asn Tyr Thr Tyr Glu Lys Ser Asn Val Glu Val  
                   180                  185                  190

*Bent*

Lys Ile Lys Glu Leu Asn Tyr Leu Lys Thr Ile Gln Asp Lys Leu Ala  
 195 200 205  
 Asp Phe Lys Lys Asn Asn Asn Phe Val Gly Ile Ala Asp Leu Ser Thr  
 210 215 220  
 Asp Tyr Asn His Asn Asn Leu Leu Thr Lys Phe Leu Ser Thr Gly Met  
 225 230 235 240  
 Val Phe Glu Asn Leu Ala Lys Thr Val Leu Ser Asn Leu Leu Asp Gly  
 245 250 255  
 Asn Leu Gln Gly Met Leu Asn Ile Ser Gln His Gln Cys Val Lys Lys  
 260 265 270  
 Gln Cys Pro Gln Asn Ser Gly Cys Phe Arg His Leu Asp Glu Arg Glu  
 275 280 285  
 Glu Cys Lys Cys Leu Leu Asn Tyr Lys Gln Glu Gly Asp Lys Cys Val  
 290 295 300  
 Glu Asn Pro Asn Pro Thr Cys Asn Glu Asn Asn Gly Gly Cys Asp Ala  
 305 310 315 320  
 Asp Ala Lys Cys Thr Glu Glu Asp Ser Gly Ser Asn Gly Lys Lys Ile  
 325 330 335  
 Thr Cys Glu Cys Thr Lys Pro Asp Ser Tyr Pro Leu Phe Asp Gly Ile  
 340 345 350  
 Phe Cys Ser  
 355

<210> 12  
 <211> 361  
 <212> PRT  
 <213> preferably, a bacterium, virus, or parasite

<400> 12  
 Ala Val Thr Pro Ser Val Ile Asp Asn Ile Leu Ser Lys Ile Glu Asn  
 1 5 10 15  
 Glu Tyr Glu Val Leu Tyr Leu Lys Pro Leu Ala Gly Val Tyr Arg Ser  
 20 25 30  
 Leu Lys Lys Gln Leu Glu Asn Asn Val Met Thr Phe Asn Val Asn Val  
 35 40 45  
 Lys Asp Ile Leu Asn Ser Arg Phe Asn Lys Arg Glu Asn Phe Lys Asn  
 50 55 60  
 Val Leu Glu Ser Asp Leu Ile Pro Tyr Lys Asp Leu Thr Ser Ser Asn  
 65 70 75 80  
 Tyr Val Val Lys Asp Pro Tyr Lys Phe Leu Asn Lys Glu Lys Arg Asp  
 85 90 95  
 Lys Phe Leu Ser Ser Tyr Asn Tyr Ile Lys Asp Ser Ile Asp Thr Asp  
 100 105 110  
 Ile Asn Phe Ala Asn Asp Val Leu Gly Tyr Tyr Lys Ile Leu Ser Glu  
 115 120 125  
 Lys Tyr Lys Ser Asp Leu Asp Ser Ile Lys Lys Tyr Ile Asn Asp Lys  
 130 135 140  
 Gln Gly Glu Asn Glu Lys Tyr Leu Pro Phe Leu Asn Asn Ile Glu Thr  
 145 150 155 160  
 Leu Tyr Lys Thr Val Asn Asp Lys Ile Asp Leu Phe Val Ile His Leu  
 165 170 175  
 Glu Ala Lys Val Leu Asn Tyr Thr Tyr Glu Lys Ser Asn Val Glu Val  
 180 185 190  
 Lys Ile Lys Glu Leu Asn Tyr Leu Lys Thr Ile Gln Asp Lys Leu Ala  
 195 200 205  
 Asp Phe Lys Lys Asn Asn Asn Phe Val Gly Ile Ala Asp Leu Ser Thr  
 210 215 220  
 Asp Tyr Asn His Asn Asn Leu Leu Thr Lys Phe Leu Ser Thr Gly Met  
 225 230 235 240  
 Val Phe Glu Asn Leu Ala Lys Thr Val Leu Ser Asn Leu Leu Asp Gly  
 245 250 255



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Leu | Gln | Gly | Met | Leu | Asn | Ile | Ser | Gln | His | Gln | Cys | Val | Lys | Lys |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gln | Cys | Pro | Gln | Asn | Ser | Gly | Cys | Phe | Arg | His | Leu | Asp | Glu | Arg | Glu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Glu | Cys | Lys | Cys | Leu | Leu | Asn | Tyr | Lys | Gln | Glu | Gly | Asp | Lys | Cys | Val |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Glu | Asn | Pro | Asn | Pro | Thr | Cys | Asn | Glu | Asn | Asn | Gly | Gly | Cys | Asp | Ala |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Asp | Ala | Lys | Cys | Thr | Glu | Glu | Asp | Ser | Gly | Ser | Asn | Gly | Lys | Lys | Ile |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Thr | Cys | Glu | Cys | Thr | Lys | Pro | Asp | Ser | Tyr | Pro | Leu | Phe | Asp | Gly | Ile |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Phe | Cys | Ser | His | His | His | His | His | His |     |     |     |     |     |     |     |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     |     |     |     |     |

&lt;210&gt; 13

&lt;211&gt; 376

&lt;212&gt; PRT

&lt;213&gt; preferably, a bacterium, virus, or parasite

&lt;400&gt; 13

*Bank*

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Val | Leu | Ile | Ile | Ala | Cys | Leu | Val | Ala | Leu | Ala | Ile | Ala | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Thr | Pro | Ser | Val | Ile | Asp | Asn | Ile | Leu | Ser | Lys | Ile | Glu | Asn | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Glu | Val | Leu | Tyr | Leu | Lys | Pro | Leu | Ala | Gly | Val | Tyr | Arg | Ser | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Lys | Gln | Leu | Glu | Asn | Asn | Val | Met | Thr | Phe | Asn | Val | Asn | Val | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Ile | Leu | Asn | Ser | Arg | Phe | Asn | Lys | Arg | Glu | Asn | Phe | Lys | Asn | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Leu | Glu | Ser | Asp | Leu | Ile | Pro | Tyr | Lys | Asp | Leu | Thr | Ser | Ser | Asn | Tyr |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Val | Lys | Asp | Pro | Tyr | Lys | Phe | Leu | Asn | Lys | Glu | Lys | Arg | Asp | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Leu | Ser | Ser | Tyr | Asn | Tyr | Ile | Lys | Asp | Ser | Ile | Asp | Thr | Asp | Ile |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Phe | Ala | Asn | Asp | Val | Leu | Gly | Tyr | Tyr | Lys | Ile | Leu | Ser | Glu | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Tyr | Lys | Ser | Asp | Leu | Asp | Ser | Ile | Lys | Lys | Tyr | Ile | Asn | Asp | Lys | Gln |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gly | Glu | Asn | Glu | Lys | Tyr | Leu | Pro | Phe | Leu | Asn | Asn | Ile | Glu | Thr | Leu |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Tyr | Lys | Thr | Val | Asn | Asp | Lys | Ile | Asp | Leu | Phe | Val | Ile | His | Leu | Glu |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Lys | Val | Leu | Gln | Tyr | Thr | Tyr | Glu | Lys | Ser | Asn | Val | Glu | Val | Lys |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ile | Lys | Glu | Leu | Asn | Tyr | Leu | Lys | Thr | Ile | Gln | Asp | Lys | Leu | Ala | Asp |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Phe | Lys | Lys | Asn | Asn | Asn | Phe | Val | Gly | Ile | Ala | Asp | Leu | Ser | Thr | Asp |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Tyr | Asn | His | Asn | Asn | Leu | Leu | Thr | Lys | Phe | Leu | Ser | Thr | Gly | Met | Val |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Phe | Glu | Asn | Leu | Ala | Lys | Thr | Val | Leu | Ser | Asn | Leu | Leu | Asp | Gly | Asn |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Leu | Gln | Gly | Met | Leu | Gln | Ile | Ser | Gln | His | Gln | Cys | Val | Lys | Lys | Gln |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Cys | Pro | Gln | Asn | Ser | Gly | Cys | Phe | Arg | His | Leu | Asp | Glu | Arg | Glu | Glu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Cys | Lys | Cys | Leu | Leu | Asn | Tyr | Lys | Gln | Glu | Gly | Asp | Lys | Cys | Val | Glu |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |

Panel.

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